

SEQUENCE LISTING

<110> Chugai Seiyaku Kabushiki Kaisha  
<120> Immunochemical Assay Method for Anti-HM 24 Antibody  
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<150> JP 10-060613  
<151> 1998-03-20  
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<213> Homosapiens  
<223> Nucleotide sequence of extracellular domain of soluble  
HM 1.24 antigenic protein

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aat gtc acc cat ctc ctg caa caa gag ctg acc gag gcc cag aag ggc 96  
Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly  
20 25 30  
ttt cag gat gtg gag gcc cag gcc gcc acc tgc aac cac act gtg atg 144  
Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met  
35 40 45  
gcc cta atg gct tcc ctg gat gca gag aag gcc caa gga caa aag aaa 192  
Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys  
50 55 60  
gtg gag gag ctt gag gga gag atc act aca tta aac cat aag ctt cag 240  
Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln  
65 70 75 80  
gac gcg tct gca gag gtg gag cga ctg aga aga gaa aac cag gtc tta 288  
Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu  
85 90 95  
agc gtg aga atc gcg gac aag aag tac tac ccc agc tcc cag gac tcc 336  
Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser  
100 105 110

agc tcc gct gcg gcg ccc cag ctg ctg att gtg ctg ctg ggc ctc agc 384  
 Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser  
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 HM 1.24 antigenic protein  
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 aca gct aca ggt gtc cac tcc gac tac aaa gac gat gac gat aaa ggt 95  
 Thr Ala Thr Gly Val His Ser Asp Tyr Lys Asp Asp Asp Asp Lys Gly  
 15 20 25  
 acc aac agc gag gcc tgc cgg gac ggc ctt cgg gca gtg atg gag tgt 143  
 Thr Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys  
 30 35 40  
 cgc aat gtc acc cat ctc ctg caa caa gag ctg acc gag gcc cag aag 191  
 Arg Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys  
 45 50 55 60  
 ggc ttt cag gat gtg gag gcc cag gcc gcc acc tgc aac cac act gtg 239  
 Gly Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val  
 65 70 75  
 atg gcc cta atg gct tcc ctg gat gca gag aag gcc caa gga caa aag 287  
 Met Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys  
 80 85 90

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aaa gtg gag gag ctt gag gga gag atc act aca tta aac cat aag ctt      335
Lys Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu
      95                      100                      105

cag gac gcg tct gca gag gtg gag cga ctg aga aga gaa aac cag gtc      383
Gln Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val
      110                      115                      120

tta agc gtg aga atc gcg gac aag aag tac tac ccc agc tcc cag gac      431
Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp
      125                      130                      135                      140

tcc agc tcc gct gcg gcg ccc cag ctg ctg att gtg ctg ctg ggc ctc      479
Ser Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu
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Ser Ala Leu Leu Gln
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<223> Nucleotide sequence coding for a fusion protein
      comprising HA peptide and soluble HM 1.24 antigenic
      protein

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Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Asn Ser Glu Ala Cys
      1                      5                      10                      15

cgg gac ggc ctt cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc      96
Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu
      20                      25                      30

ctg caa caa gag ctg acc gag gcc cag aag ggc ttt cag gat gtg gag      144
Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu
      35                      40                      45

gcc cag gcc gcc acc tgc aac cac act gtg atg gcc cta atg gct tcc      192
Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser
      50                      55                      60

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ctg gat gca gag aag gcc caa gga caa aag aaa gtg gag gag ctt gag	240
Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu	
65 70 75 80	
gga gag atc act aca tta aac cat aag ctt cag gac gcg tct gca gag	288
Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu	
85 90 95	
gtg gag cga ctg aga aga gaa aac cag gtc tta agc gtg aga atc gcg	336
Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala	
100 105 110	
gac aag aag tac tac ccc agc tcc cag gac tcc agc tcc gct gcg gcg	384
Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala	
115 120 125	
ccc cag ctg ctg att gtg ctg ctg ggc ctc agc gct ctg ctg cag	429
Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln	
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<212> DNA	
<213> Artificial Sequence	
<223> Nucleotide sequence coding for a fusion protein	
comprising HA peptide and C-terminal-lacking soluble	
HM 1.24 antigenic protein	
<400> 4	
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Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Asn Ser Glu Ala Cys	
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cgg gac ggc ctt cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc	96
Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu	
20 25 30	
ctg caa caa gag ctg acc gag gcc cag aag ggc ttt cag gat gtg gag	144
Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu	
35 40 45	
gcc cag gcc gcc acc tgc aac cac act gtg atg gcc cta atg gct tcc	192
Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser	
50 55 60	

ctg gat gca gag aag gcc caa gga caa aag aaa gtg gag gag ctt gag	240
Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu	
65 70 75 80	
gga gag atc act aca tta aac cat aag ctt cag gac gcg tct gca gag	288
Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu	
85 90 95	
gtg gag cga ctg aga aga gaa aac cag gtc tta agc gtg aga atc gcg	336
Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala	
100 105 110	
gac aag aag tac tac ccc agc tcc cag gac tcc agc tcc gct	378
Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala	
115 120 125	
tgaggatcc	387
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<223> Nucleotide sequence coding for CG M/HA-HM164	
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Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu	
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ctc tgg ctc cca ggt gca cga tgt gca tac cca tac gac gtc cca gac	96
Leu Trp Leu Pro Gly Ala Arg Cys Ala Tyr Pro Tyr Asp Val Pro Asp	
15 20 25	
tac gct ggt acc aac agc gag gcc tgc cgg gac ggc ctt cgg gca gtg	144
Tyr Ala Gly Thr Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val	
30 35 40	
atg gag tgt cgc aat gtc acc cat ctc ctg caa caa gag ctg acc gag	192
Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu	
45 50 55 60	
gcc cag aag ggc ttt cag gat gtg gag gcc cag gcc gcc acc tgc aac	240
Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn	
65 70 75	
cac act gtg atg gcc cta atg gct tcc ctg gat gca gag aag gcc caa	288
His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln	
80 85 90	
gga caa aag aaa gtg gag gag ctt gag gga gag atc act aca tta aac	336
Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn	
95 100 105	
cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg aga aga gaa	384
His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu	
110 115 120	
aac cag gtc tta agc gtg aga atc gcg gac aag aag tac tac ccc agc	432
Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser	
125 130 135 140	
tcc cag gac tcc agc tcc gct tgaggatcct atggttacca actacctaga	483
Ser Gln Asp Ser Ser Ser Ala	
145	
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 <223> Primer  
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 <223> Primer  
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 <211> 106  
 <212> DNA  
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<220>  
 <223> Synthetic DNA comprising leader sequence and FLAG  
 coding sequence  
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 ccactccgac taaaagacg atgacgataa aggtaccgcg gccgcg 106  
 <210> 13  
 <211> 106  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic DNA comprising leader sequence and FLAG  
 coding sequence  
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 ctgttgctac caagaagagg atgatacagc tccatcccat ggtggg 106  
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 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic DNA coding for HA peptide  
 <400> 14  
 gtgcataccc atacgacgtc ccagactacg ctggtac 37  
 <210> 15  
 <211> 36  
 <212> DNA  
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 <223> Synthetic DNA coding for HA peptide  
 <400> 15  
 cagcgtagtc tgggacgctg tatgggtatg cacatc 36  
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<213> Homosapiens

<223> Nucleotide sequence coding for humam HM 1.24 antigenic protein expressed on cell membrane

<400> 16

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Arg Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly
      10              15              20              25
ata gga att ctg gtg ctc ctg atc atc gtg att ctg ggg gtg ccc ttg      145
Ile Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu
              30              35              40
att atc ttc acc atc aag gcc aac agc gag gcc tgc cgg gac ggc ctt      193
Ile Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu
              45              50              55
cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc ctg caa caa gag      241
Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu
              60              65              70
ctg acc gag gcc cag aag ggc ttt cag gat gtg gag gcc cag gcc gcc      289
Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala
              75              80              85
acc tgc aac cac act gtg atg gcc cta atg gct tcc ctg gat gca gag      337
Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu
              90              95              100              105
aag gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act      385
Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr
              110              115              120
aca tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg      433
Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu
              125              130              135
aga aga gaa aac cag gtc tta agc gtg aga atc gcg gac aag aag tac      481
Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr
              140              145              150
tac ccc agc tcc cag gac tcc agc tcc gct gcg gcg ccc cag ctg ctg      529
Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala Pro Gln Leu Leu
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 ttctgagcgg gtcattggggc aacacgggta gcggggagag cacggggtag ccggagaagg 702  
 gcctctggag caggtctgga gggggccatgg ggcagtcctg ggtgtgggga cacagtcggg 762  
 ttgaccacagg gctgtctccc tccagagcct ccctccggac aatgagtccc ccctcttgtc 822  
 tcccaccctg agattgggca tgggggtgcgg tgtggggggc atgtgctgcc tgttgttatg 882  
 ggtttttttt gcggggggggg ttgctttttt ctgggggtctt tgagctccaa aaaaataaac 942  
 acttcctttg agggagagca caccttaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaatc 1002  
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 Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
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 gtc cac tcc gac atc cag atg acc cag agc cca agc agc ctg agc gcc 96  
 Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
 -1 1 5 10  
 agc gtg ggt gac aga gtg acc atc acc tgt aag gct agt cag gat gtg 144  
 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val  
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 aat act gct gta gcc tgg tac cag cag aag cca gga aag gct cca aag 192  
 Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
 30 35 40 45  
 ctg ctg atc tac tgg gca tcc aac cgg tac act ggt gtg cca agc aga 240  
 Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg  
 50 55 60  
 ttc agc ggt agc ggt agc ggt acc gac ttc acc ttc acc atc agc agc 288  
 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
 65 70 75

ctc cag cca gag gac atc gct acc tac tac tgc cag caa cat tat agt	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser	
80 85 90	
act cca ttc acg ttc ggc caa ggg acc aag gtg gaa atc aaa c	379
Thr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
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<223> Nucleotide sequence coding for H chain V region	
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gct cac tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag	96
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
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cct ggg gcc tca gtg aag gtt tcc tgc aag gca tct gga tac acc ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
15 20 25	
act ccc tac tgg atg cag tgg gtg cga cag gcc cct gga caa ggg ctt	192
Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu	
30 35 40 45	
gag tgg atg gga tct att ttt cct gga gat ggt gat act agg tac agt	240
Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser	
50 55 60	
cag aag ttc aag ggc aga gtc acc atg acc gca gac aag tcc acg agc	288
Gln Lys Phe Lys Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser	
65 70 75	
aca gcc tac atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
80 85 90	

tat tac tgt gcg aga gga tta cga cga ggg ggg tac tac ttt gac tac	384
Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr	
95 100 105	
tgg ggg caa ggg acc acg gtc acc gtc tcc tca g	418
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser	
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<223> Nucleotide sequence coding for H chain V region	
version s of humanized anti-HM 1.24 antibody	
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gct cac tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag	96
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
-1 1 5 10	
cct ggg gcc tca gtg aag gtt tcc tgc aag gca tct gga tac acc ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
15 20 25	
act ccc tac tgg atg cag tgg gtg cga cag gcc cct gga caa ggg ctt	192
Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu	
30 35 40 45	
gag tgg atg gga tct att ttt cct gga gat ggt gat act agg tac agt	240
Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser	
50 55 60	
cag aag ttc aag ggc aga gtc acc atc acc gca gac aag tcc acg agc	288
Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser	
65 70 75	
aca gcc tac atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
80 85 90	

tat tac tgt gcg aga gga tta cga cga ggg ggg tac tac ttt gac tac 384  
 Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr  
           95                          100                          105

tgg ggg caa ggg acc acg gtc acc gtc tcc tca g 418  
 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
 110                          115                          120

<210> 20

<211> 132

<212> PRT

<213> Homosapiens

<223> Amino acid sequence of soluble HM 1.24 antigenic  
           protein

<400> 20

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Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly  
                           20                          25                          30

Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met  
           35                          40                          45

Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys  
           50                          55                          60

Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln  
       65                          70                          75                          80

Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu  
                           85                          90                          95

Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser  
                           100                          105                          110

Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser  
           115                          120                          125

Ala Leu Leu Gln  
           130

<210> 21

<211> 161

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of a fusion protein comprising  
leader sequence, FLAG peptide and soluble HM 1.24  
antigenic protein

<400> 21

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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
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             20             25             30
Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr
             35             40             45
His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp
             50             55             60
Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met
             65             70             75             80
Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu
             85             90             95
Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln Asp Ala Ser
             100            105            110
Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu Ser Val Arg
             115            120            125
Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala
             130            135            140
Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser Ala Leu Leu
             145            150            155            160
Gln

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<210> 22

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<212> PRT

<213> Artificial Sequence

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<223> Amino acid sequence of a fusion protein comprising HA  
peptide and soluble HM 1.24 antigenic protein

<400> 22

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Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Asn Ser Glu Ala Cys
  1             5             10             15
Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu
             20             25             30

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Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu  
                   35                                  40                                  45  
 Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser  
                   50                                  55                                  60  
 Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu  
                   65                                  70                                  75                                  80  
 Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu  
                                   85                                  90                                  95  
 Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala  
                   100                                  105                                  110  
 Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala  
                   115                                  120                                  125  
 Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln  
                   130                                  135                                  140

<210> 23

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of a fusion protein comprising HA  
 peptide and C-terminal lacking soluble HM 1.24  
 antigenic protein

<400> 23

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Asn Ser Glu Ala Cys  
           1                                  5                                  10                                  15  
 Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu  
                   20                                  25                                  30  
 Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu  
                   35                                  40                                  45  
 Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser  
                   50                                  55                                  60  
 Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu  
                   65                                  70                                  75                                  80  
 Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu  
                                   85                                  90                                  95  
 Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala  
                   100                                  105                                  110

Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala  
115 120 125

<210> 24

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of HA peptide

<400> 24

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala

1 5

<210> 25

<211> 147

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of CGM/HA-HM164

<400> 25

Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp Leu pro

1 5 10 15

Gly Ala Arg Cys Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr

20 25 30

Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg

35 40 45

Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly

50 55 60

Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met

65 70 75 80

Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys

85 90 95

Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln

100 105 110

Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu

115 120 125

Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser

130 135 140



Ser Ser Ala

145

<210> 26

<211> 180

<212> PRT

<213> Homosapiens

<223> Amino acid sequence of humam HM 1.24 antigenic protein  
expressed on cell membrane

<400> 26

Met	Ala	Ser	Thr	Ser	Tyr	Asp	Tyr	Cys	Arg	Val	Pro	Met	Glu	Asp	Gly
1				5					10					15	
Asp	Lys	Arg	Cys	Lys	Leu	Leu	Leu	Gly	Ile	Gly	Ile	Leu	Val	Leu	Leu
			20					25					30		
Ile	Ile	Val	Ile	Leu	Gly	Val	Pro	Leu	Ile	Ile	Phe	Thr	Ile	Lys	Ala
			35				40					45			
Asn	Ser	Glu	Ala	Cys	Arg	Asp	Gly	Leu	Arg	Ala	Val	Met	Glu	Cys	Arg
	50					55					60				
Asn	Val	Thr	His	Leu	Leu	Gln	Gln	Glu	Leu	Thr	Glu	Ala	Gln	Lys	Gly
	65				70				75					80	
Phe	Gln	Asp	Val	Glu	Ala	Gln	Ala	Ala	Thr	Cys	Asn	His	Thr	Val	Met
			85					90					95		
Ala	Leu	Met	Ala	Ser	Leu	Asp	Ala	Glu	Lys	Ala	Gln	Gly	Gln	Lys	Lys
		100					105					110			
Val	Glu	Glu	Leu	Glu	Gly	Glu	Ile	Thr	Thr	Leu	Asn	His	Lys	Leu	Gln
		115				120						125			
Asp	Ala	Ser	Ala	Glu	Val	Glu	Arg	Leu	Arg	Arg	Glu	Asn	Gln	Val	Leu
	130					135					140				
Ser	Val	Arg	Ile	Ala	Asp	Lys	Lys	Tyr	Tyr	Pro	Ser	Ser	Gln	Asp	Ser
	145				150					155				160	
Ser	Ser	Ala	Ala	Ala	Pro	Gln	Leu	Leu	Ile	Val	Leu	Leu	Gly	Leu	Ser
			165					170					175		
Ala	Leu	Leu	Gln												
			180												

<210> 27

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of L chain V region version a of  
humanized amti-HM 1.24 antibody

<400> 27

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Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
          -15                -10                -5
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
      -1  1                5                10
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val
      15                20                25
Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
      30                35                40                45
Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg
          50                55                60
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
          65                70                75
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser
          80                85                90
Thr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
          95                100                105
```

<210> 28

<211> 139

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of H chain V region version r of  
humanized anti-HM 1.24 antibody

<400> 28

```
Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly
          -15                -10                -5
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
      -1  1                5                10
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
      15                20                25
Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
      30                35                40                45
```

Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser  
                             50                            55                            60  
 Gln Lys Phe Lys Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser  
                             65                            70                            75  
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
                             80                            85                            90  
 Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr  
                             95                            100                            105  
 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
 110                            115                            120

<210> 29

<211> 139

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of H chain V region version s of  
humanized anti-HM 1.24 antibody

<400> 29

Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly  
                             -15                            -10                            -5  
 Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
                             -1    1                            5                            10  
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
                             15                            20                            25  
 Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
                             30                            35                            40                            45  
 Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser  
                             50                            55                            60  
 Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser  
                             65                            70                            75  
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
                             80                            85                            90  
 Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr  
                             95                            100                            105  
 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
 110                            115                            120